Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 03:18:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004125.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6004125 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004125.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 03:18:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004125.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,552,071
Mapped reads	2,309,520 / 90.5%
Unmapped reads	242,551 / 9.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,868 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	113,489 / 4.45%
Duplication rate	3.33%
Clipped reads	1,306,013 / 51.17%

2.2. ACGT Content

Number/percentage of A's	38,906,190 / 26.37%
Number/percentage of C's	28,674,849 / 19.43%
Number/percentage of T's	44,108,885 / 29.89%
Number/percentage of G's	35,853,726 / 24.3%
Number/percentage of N's	19,146 / 0.01%
GC Percentage	43.73%

2.3. Coverage

Mean	0.0477

Standard Deviation	0.5124

2.4. Mapping Quality

Mean Mapping Quality	40.55

2.5. Mismatches and indels

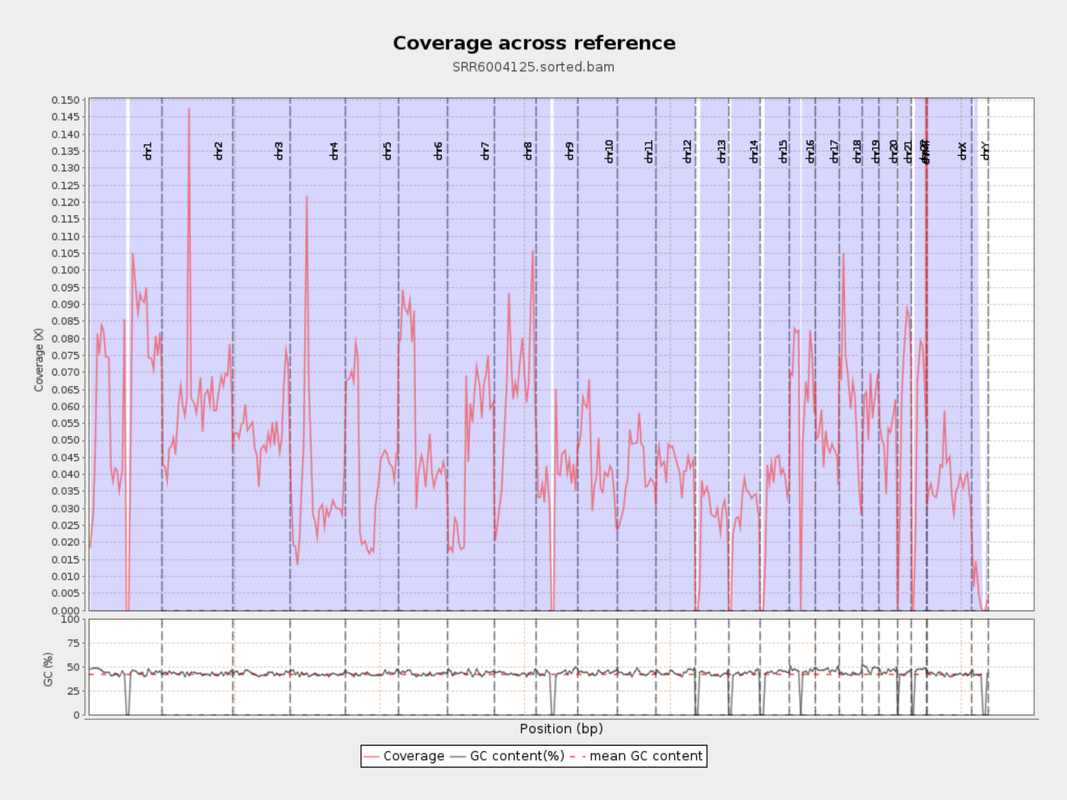
General error rate	0.95%
Mismatches	1,376,751
Insertions	12,637
Mapped reads with at least one insertion	0.54%
Deletions	42,161
Mapped reads with at least one deletion	1.81%
Homopolymer indels	46.94%

2.6. Chromosome stats

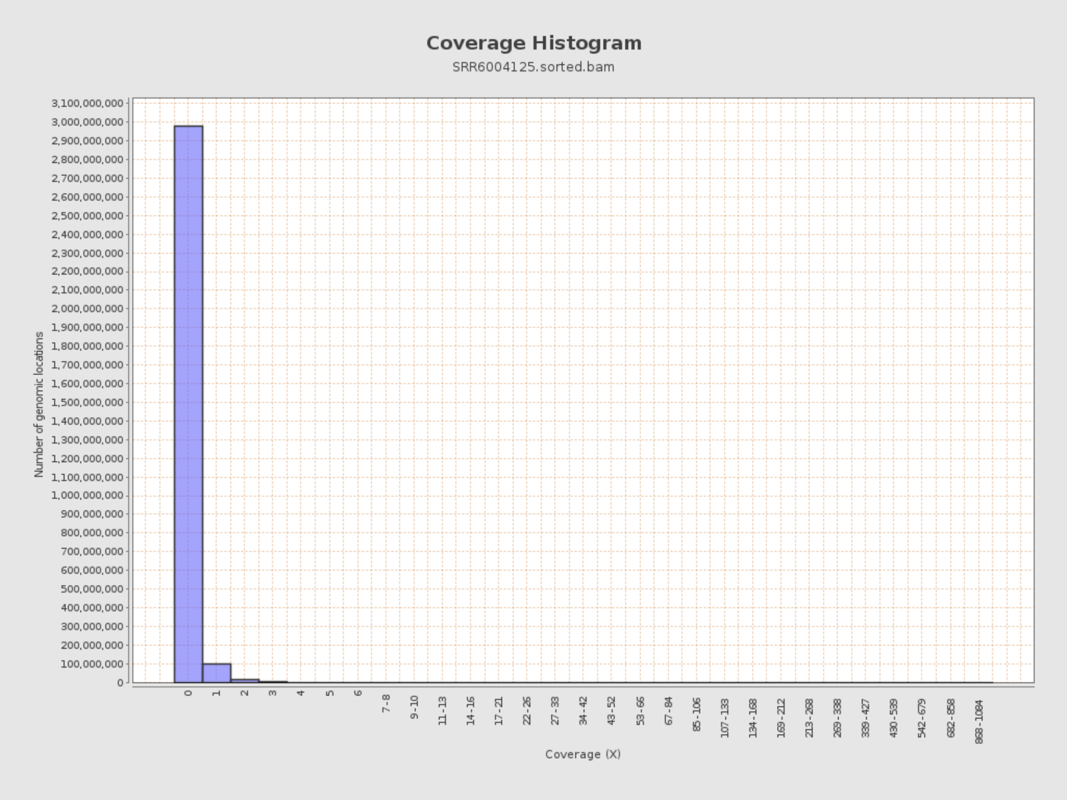
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16016827	0.0643	0.7883
chr2	243199373	15146329	0.0623	0.8788
chr3	198022430	10536767	0.0532	0.2799
chr4	191154276	6630946	0.0347	0.2403
chr5	180915260	7733688	0.0427	0.2576
chr6	171115067	9690731	0.0566	0.3873
chr7	159138663	7531870	0.0473	0.5488

chr8	146364022	9207699	0.0629	0.522
chr9	141213431	5106079	0.0362	0.5419
chr10	135534747	6078201	0.0448	0.37
chr11	135006516	5487360	0.0406	0.4327
chr12	133851895	5750763	0.043	0.2652
chr13	115169878	2946660	0.0256	0.189
chr14	107349540	2922667	0.0272	0.3348
chr15	102531392	3359333	0.0328	0.2299
chr16	90354753	5852765	0.0648	0.3529
chr17	81195210	3936103	0.0485	0.3427
chr18	78077248	5000279	0.064	1.2141
chr19	59128983	3621919	0.0613	0.683
chr20	63025520	3219077	0.0511	0.3191
chr21	48129895	2997422	0.0623	0.3323
chr22	51304566	2523240	0.0492	0.2749
chrMT	16571	103925	6.2715	7.6995
chrX	155270560	5918914	0.0381	0.3568
chrY	59373566	313468	0.0053	0.111

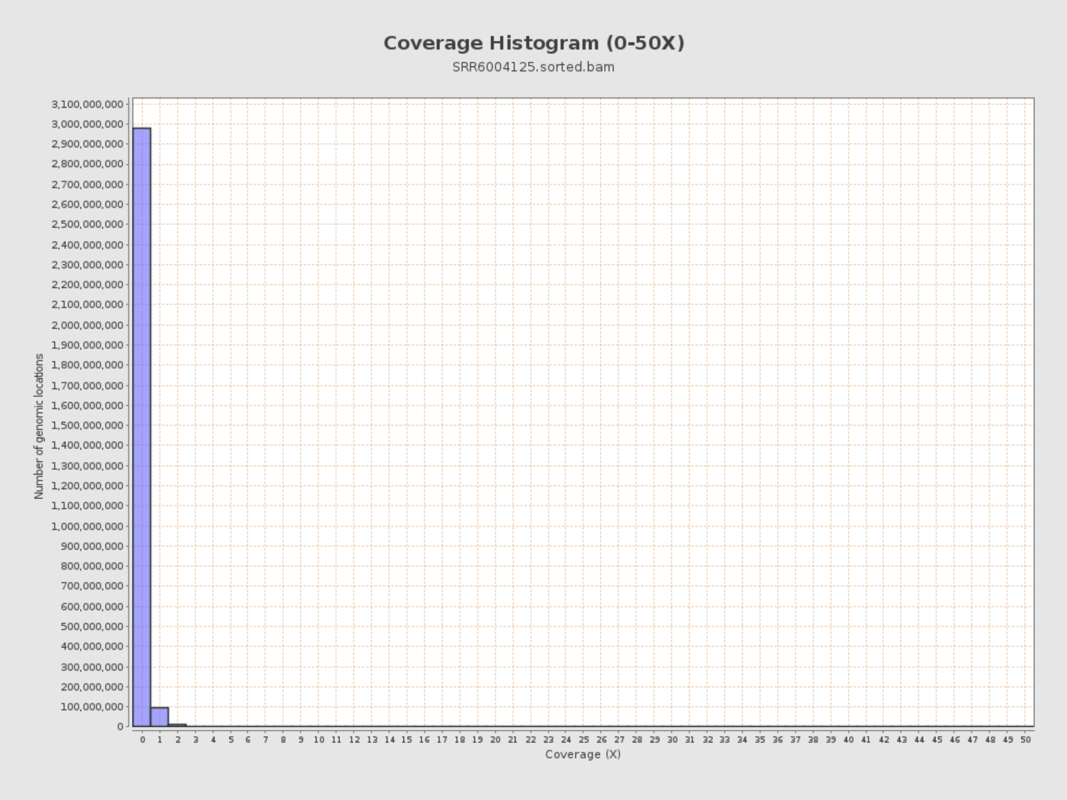
3. Results : Coverage across reference



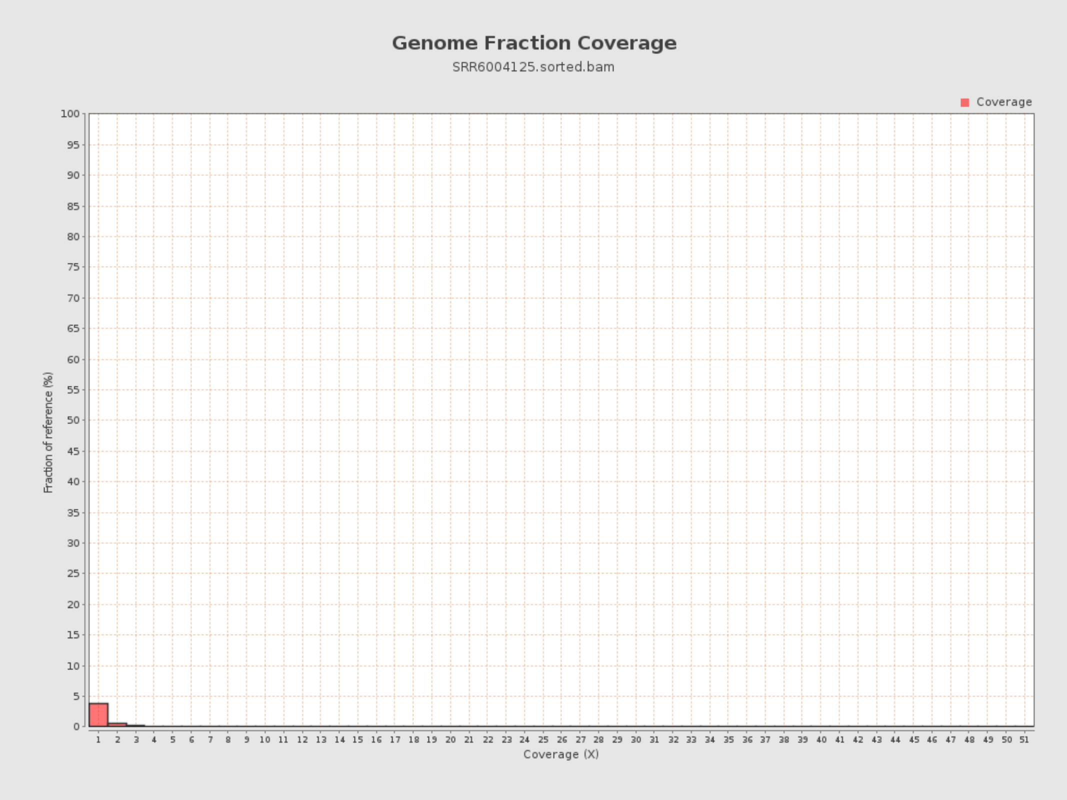
4. Results : Coverage Histogram



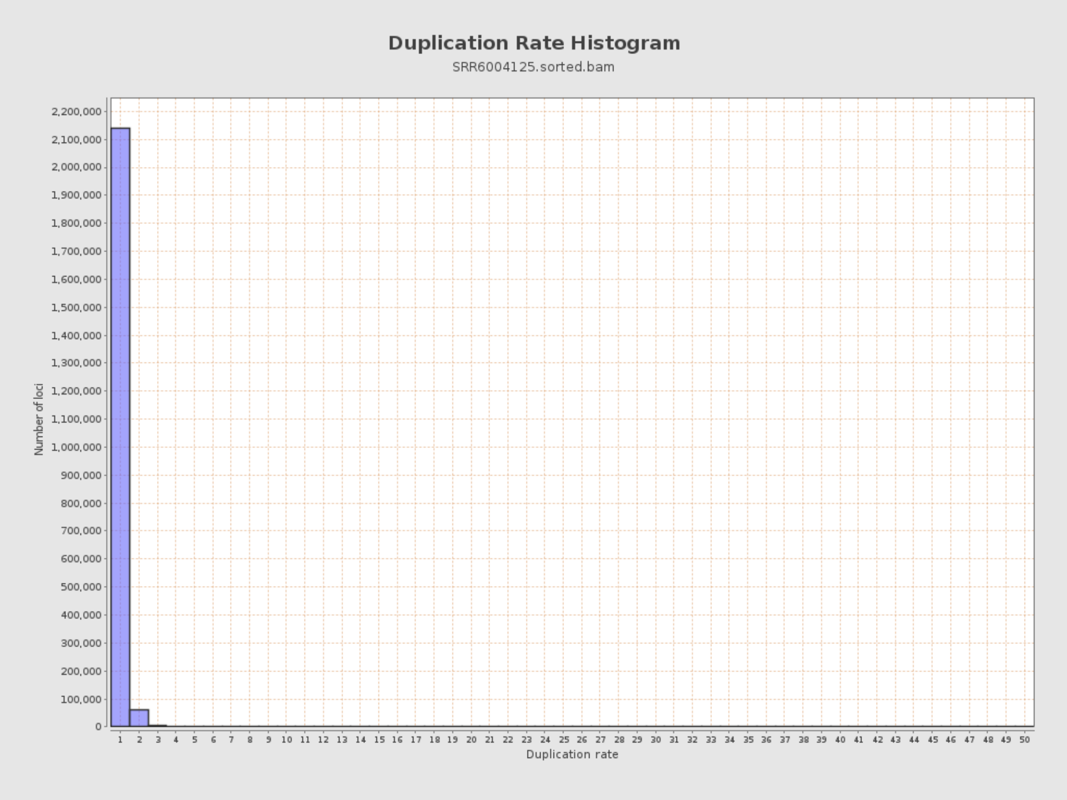
5. Results : Coverage Histogram (0-50X)



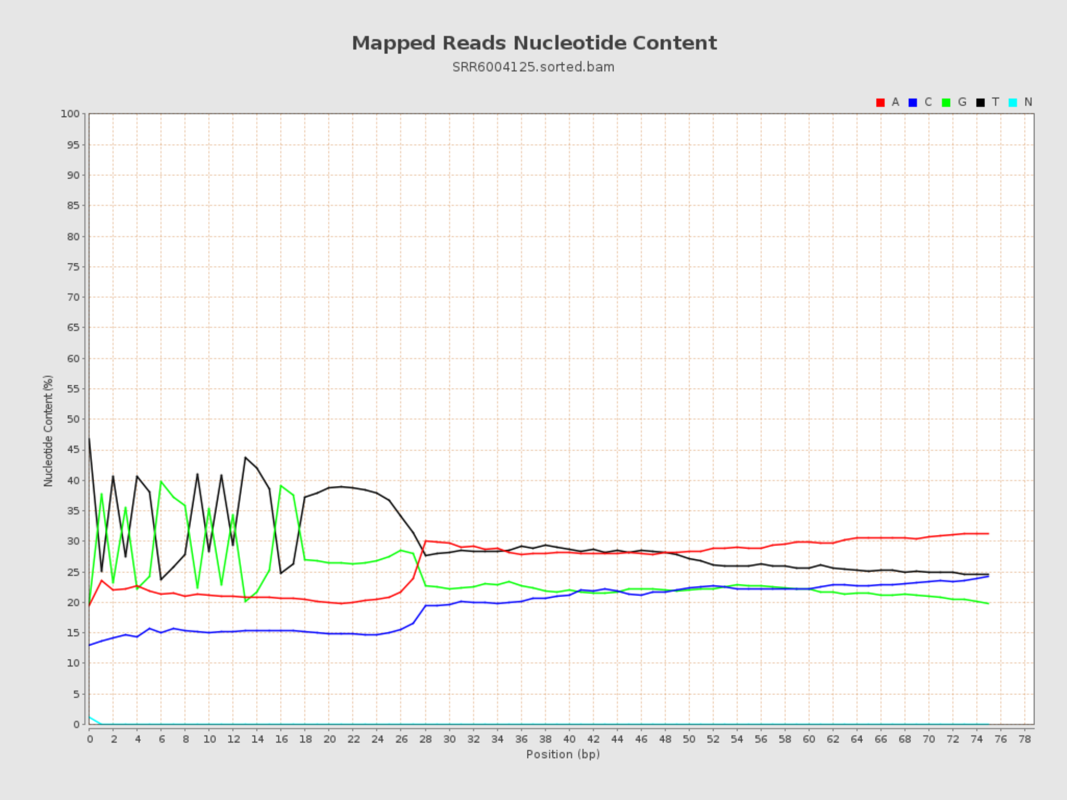
6. Results : Genome Fraction Coverage



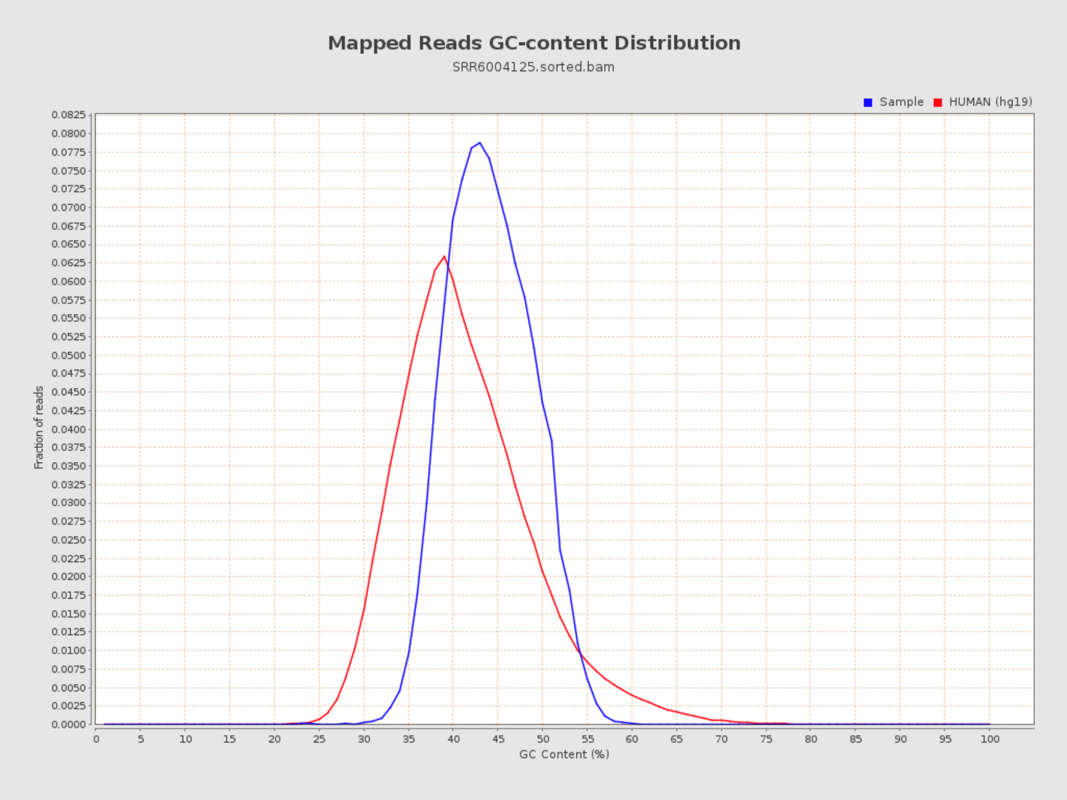
7. Results : Duplication Rate Histogram



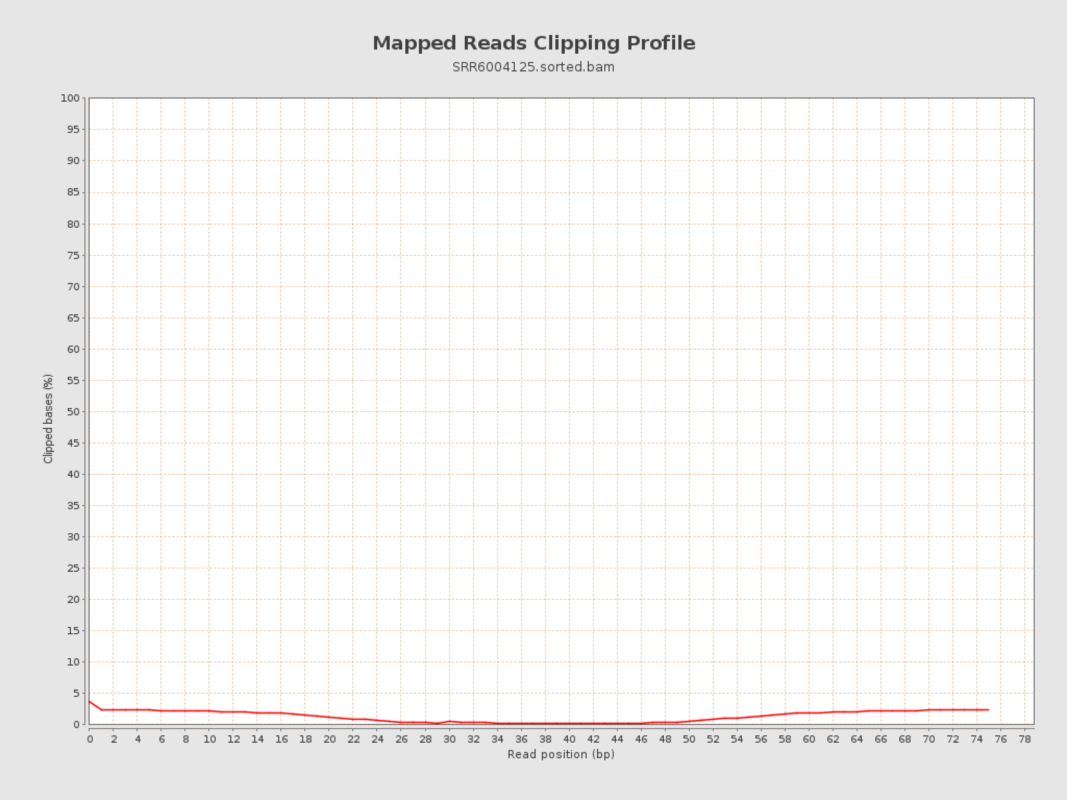
8. Results : Mapped Reads Nucleotide Content



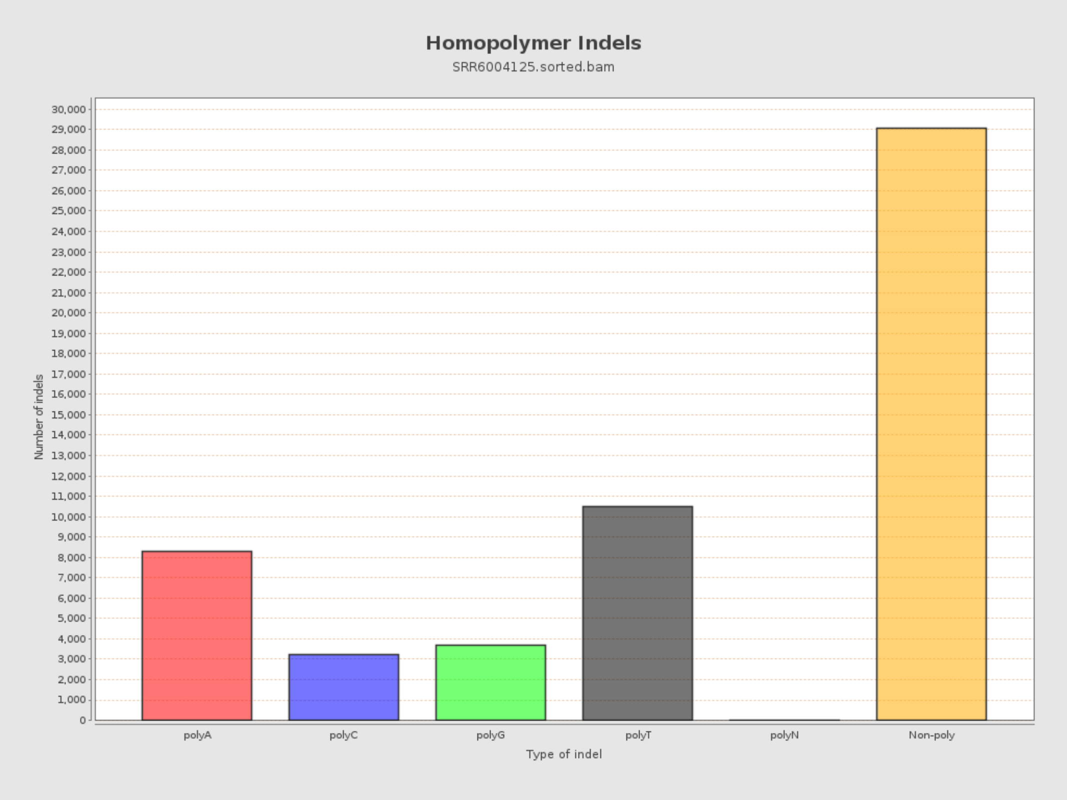
9. Results : Mapped Reads GC-content Distribution



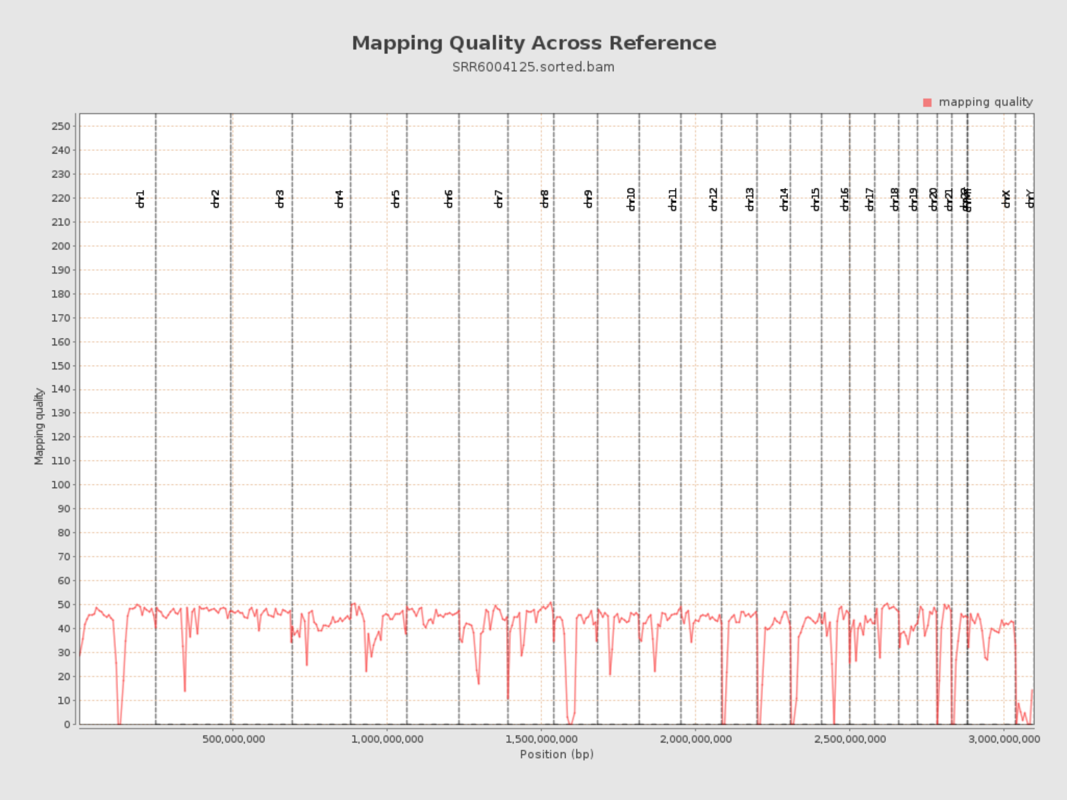
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram